

| GenCore version 4.5 | c 28 | 19.6 | 2.0 | Sequence 174, APP |
|--|-------|--------------|---------------------------|-------------------|
| Copyright (c) 1993 - 2000 Compugen Ltd. | c 29 | 19.6 | 2.0 | Sequence 62, APP |
| OM nucleic - nucleic search, using sw model | c 30 | 19.6 | 2.0 | Sequence 174, APP |
| Run on: April 17, 2002, 01:23:59 : Search time 86.07 Seconds (without alignments) | c 31 | 19.6 | 2.0 | Sequence 19, APP |
| | c 32 | 19.6 | 2.0 | Sequence 20, APP |
| Title: US-09-439-311-1 | c 33 | 19.6 | 2.0 | Sequence 2, APP |
| Perfect score: 999 | c 34 | 19.4 | 1.9 | Sequence 8, APP |
| Sequence: 1 attaaacaaaatgttcgac.....ttaaaaatgttcggatagat 999 | c 35 | 19.4 | 1.9 | Sequence 127, APP |
| Scoring table: IDENTITY_NUC | c 36 | 19.4 | 1.9 | Sequence 127, APP |
| Gapop 10.0 , Gapext 1.0 | c 37 | 19.4 | 1.9 | Sequence 127, APP |
| Searched: 351203 seqs. 113238999 residues | c 38 | 19.4 | 1.9 | Sequence 127, APP |
| Total number of hits satisfying chosen parameters: 515362 | c 39 | 19.4 | 1.9 | Sequence 127, APP |
| Minimum DB seq length: 0 | c 40 | 19.4 | 1.9 | Sequence 127, APP |
| Maximum DB seq length: 60 | c 41 | 19.4 | 1.9 | Sequence 127, APP |
| Post-Processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries | c 42 | 19.2 | 1.9 | Sequence 6, APP |
| Database : Issued_Patents_NA:* | c 43 | 19.2 | 1.9 | Sequence 72, APP |
| 1: /cgn2_6/pctdata/2/lna/5A_COMB_seq:* | c 44 | 19.2 | 1.9 | Sequence 72, APP |
| 2: /cgn2_6/pctdata/2/lna/5B_COMB_seq:* | c 45 | 19.2 | 1.9 | Sequence 72, APP |
| 3: /cgn2_6/pctdata/2/lna/6A_COMB_seq:* | | | | Sequence 72, APP |
| 4: /cgn2_6/pctdata/2/lna/6B_COMB_seq:* | | | | Sequence 72, APP |
| 5: /cgn2_6/pctdata/2/lna/PCTRUS_COMB_seq:* | | | | Sequence 72, APP |
| 6: /cgn2_6/pctdata/2/lna/backfill1.seq:* | | | | Sequence 72, APP |
| Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. | | | | |
| SUMMARIES | | | | |
| Result No. | Score | Query Length | DB ID | Description: |
| c 1 | 26.8 | 2.7 | 30 4 US-09-358-972-102 | Sequence 102, APP |
| c 2 | 26.8 | 2.7 | 30 4 US-09-358-972-103 | Sequence 103, APP |
| c 3 | 26.8 | 2.7 | 30 4 US-09-358-972-106 | Sequence 32, APP |
| c 4 | 26.8 | 2.7 | 30 4 US-09-358-972-147-34 | Sequence 34, APP |
| c 5 | 20.8 | 2.1 | 24 1 US-09-587-209-6 | Sequence 6, APP |
| c 6 | 20.8 | 2.1 | 24 1 US-09-689-236-6 | Sequence 6, APP |
| c 7 | 20.8 | 2.1 | 24 1 US-09-689-235-6 | Sequence 6, APP |
| c 8 | 20.8 | 2.1 | 24 1 US-09-692-725-6 | Sequence 6, APP |
| c 9 | 20.8 | 2.1 | 24 2 US-09-692-726-6 | Sequence 6, APP |
| c 10 | 20.8 | 2.1 | 58 2 US-09-431-522A-7 | Sequence 7, APP |
| c 11 | 20.8 | 2.1 | 58 4 US-09-214-278-30 | Sequence 30, APP |
| c 12 | 20.6 | 2.1 | 52 3 US-09-886-967-3 | Sequence 3, APP |
| c 13 | 20.6 | 2.1 | 52 4 US-09-306-949-3 | Sequence 3, APP |
| c 14 | 20 | 2.0 | 39 3 US-09-874-825-118 | Sequence 118, APP |
| c 15 | 20 | 2.0 | 50 2 US-09-450-903B-7 | Sequence 7, APP |
| c 16 | 20 | 2.0 | 50 3 US-09-1982-759F-7 | Sequence 4, APP |
| c 17 | 20 | 2.0 | 57 1 US-09-141-892A-4 | Sequence 4, APP |
| c 18 | 20 | 2.0 | 57 2 US-09-583-447A-4 | Sequence 4, APP |
| c 19 | 20 | 2.0 | 57 2 US-09-146-920-4 | Sequence 4, APP |
| c 20 | 20 | 2.0 | 57 3 US-09-635-930-4 | Sequence 4, APP |
| c 21 | 20 | 2.0 | 57 3 US-09-193-997-4 | Sequence 4, APP |
| c 22 | 20 | 2.0 | 57 4 US-09-138-237F-4 | Sequence 4, APP |
| c 23 | 20 | 2.0 | 60 1 US-09-478-320-4 | Sequence 4, APP |
| c 24 | 19.6 | 2.0 | 43 1 US-09-959-946-12 | Sequence 12, APP |
| c 25 | 19.6 | 2.0 | 43 5 PCT-US92-0863A-12 | Sequence 12, APP |
| c 26 | 19.6 | 2.0 | 58 1 US-09-105-483-174 | Sequence 174, APP |
| c 27 | 19.6 | 2.0 | | |

ALIGNMENTS

RESULT 1
US-09-358-972-102/c
; Sequence 102, Application US/093589972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W.
; APPLICANT: Lewis, Martin K.
; APPLICANT: Liepppe, Donna K.
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Harrnett, James R.
; APPLICANT: Olson, Trent
; APPLICANT: Hord, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: PRO-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09-358,972
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 102
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: probe to Campylobacter jejuni
US-09-358-972-102

Query Match 209 2.7%; Score 26.8; DB 4; Length 30;
Best Local Similarity 93.3%; Pred. No. 82;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 289 caggatgtcaatgttaataatccatcatact 318
Db 30 CAGATGGACAGATTTAAACAGAACCT 1

RESULT 2
US-09-358-972-103
; Sequence 103, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:

Qy 91 ggctttagaatcaactccggcga 114
 Db 24 GGTCTTAACTTAACTCAGCAGCA 1

RESULT 13
 AAV25941/C
 ID AAV25941 standard; DNA; 24 BP.
 XX
 AC AAV25941;
 XX
 DT 15-JUL-1998 (first entry)
 DE Oligonucleotide PCR primer CFO4R gene.
 XX
 KW Sequence-specific probe; enterohaemorrhagic Escherichia coli;
 Salmonella; Campylobacter; Shigella; Yersinia; beta-globin;
 KW gastroenteritis; PCR primer; ss.
 XX
 OS Synthetic.
 OS Campylobacter sp.
 XX
 PN US575344-A.
 XX
 PD 19-MAY-1998.
 XX
 PF 07-AUG-1996; 96US-0688235.
 XX
 PR 16-JAN-1996; 96US-0587209.
 PR 07-AUG-1996; 96US-0688235.
 XX
 PA (GULL-) GULL LAB INC.
 PI Coombs J, Glass MJ, Malmstrom SP, Wu L;
 WPI; 1998-260031/23.

PT Distinguishing between similar nucleic acid samples - using
 PT sequence-specific probes e.g. between enterohaemorrhagic and normal
 PT Escherichia coli

XX
 PS Example 3; Column 17: 21pp; English.

XX
 The present sequence represents a PCR primer used in an example of the
 present invention. The present invention describes a method for
 detecting mismatches between first and second nucleic acid sequences
 having at least one base difference. The method comprises: (a) obtaining
 at least one labelled probe consisting of an oligonucleotide sequence
 spanning the location of at least one base difference between the first
 and second sequences, where the oligonucleotide sequence contains at
 least one neutral base molecule in a position other than the position of
 the base difference(s) but is otherwise exactly complementary to the
 first sequence, so that the probe hybridises more weakly with the first
 sequence than with the second sequence; (b) mixing the probe(s) with the
 first and second sequences under hybridisation conditions; (c)
 dissociating any probe/second sequence hybrids; and (d) detecting
 probe/first sequence hybrids. The method can be used to distinguish
 between similar DNA/RNA sequences in a sample, especially to distinguish
 enterohaemorrhagic E. coli O157:H7 from other E. coli strains e.g. in
 stool samples from people suffering from gastroenteritis, caused
 specifically by enterohaemorrhagic E.coli. Use of the method shortens
 the time between sample preparation to obtaining results, than has been
 possible with previous similar procedures.

XX
 SQ Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 other;

Qy 91 ggctttagaatcaactccggcga 114
 Db 24 GGTCTTAACTTAACTCAGCAGCA 1

RESULT 14
 AAV20847/C
 ID AAV20847 standard; DNA; 24 BP.
 XX
 AC AAV20847;
 XX
 DT 01-JUL-1998 (first entry)
 DE Campylobacter CFO4R gene PCR primer.
 XX
 Escherichia coli strain O157:H7; detection; microorganism; infection;
 KW enterohaemorrhagic; PCR primer; ss.
 KW Synthetic.
 OS Campylobacter sp.
 OS Campylobacter sp.
 PN US5730995-A.
 XX
 PD 14-APR-1998.
 XX
 PF 07-AUG-1996; 96US-0689236.
 XX
 PR 16-JAN-1996; 96US-0587209.
 PR 07-AUG-1996; 96US-0689236.
 XX
 PA (GULL-) GULL LAB INC.
 PI Coombs J, Glass MJ, Malmstrom SP, Wu L;
 WPI; 1998-260031/23.

PT Probes for detecting Escherichia coli strain O157:H7 - useful for
 PT diagnosis of enterohaemorrhagic Escherichia coli infection(s).

XX
 PS Example 3; Column 17: 21pp; English.

XX
 The present sequence represents a PCR primer used in an example of the
 present invention. The present invention describes probes used in the
 detection of Escherichia coli strain O157:H7 in a sample. The method of
 detection comprises: (a) obtaining at least 1 probe specifically given
 in the specification, labelled with a label, that permits probe detection
 when hybridised to a complementary nucleic acid sequence which is
 specific for a nucleic acid sequence of the microorganism; (b)
 hybridising the probes and the sample, and (c) detecting hybrids
 comprising the probes and the nucleic acid sequences. The method and
 probes may be used for diagnosis of enterohaemorrhagic E. coli
 infections. The methods and the materials permit the detection and
 discrimination of multiple analytes.

XX
 SQ Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 other;

Qy 91 ggctttagaatcaactccggcga 114
 Db 24 GGTCTTAACTTAACTCAGCAGCA 1

RESULT 15
 AAF16711
 ID AAF16711 standard; DNA: 44 BP.
 XX
 AC AAF16711;
 XX
 DT 09-MAR-2001 (first entry)

Query Match 2.1%; Score 20.8; DB 19; Length 24;
 Best Local Similarity 91.7%; Pred. No. 3.4e+04;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 91 ggctttagaatcaactccggcga 114
 Db 24 GGTCTTAACTTAACTCAGCAGCA 1

Query Match 2.1%; Score 20.8; DB 19; Length 24;
 Best Local Similarity 91.7%; Pred. No. 3.4e+04;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 91 ggctttagaatcaactccggcga 114

